

## SEQUENCE LISTING

## (1) GENERAL INFORMATION

- (i) APPLICANT: Goli, Surya K.  
Hillman, Jennifer L.  
Murry, Lynn E.
- (ii) TITLE OF THE INVENTION: NOVEL HUMAN CYTOKINE/STEROID  
RECEPTOR PROTEIN
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
  - (B) STREET: 3174 Porter Drive
  - (C) CITY: Palo Alto
  - (D) STATE: CA
  - (E) COUNTRY: US
  - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Billings, Lucy J
  - (B) REGISTRATION NUMBER: 36,749
  - (C) REFERENCE/DOCKET NUMBER: PF-0233 US
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 415-855-0555
  - (B) TELEFAX: 415-845-4166
  - (C) TELEX:

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 220 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (vi) IMMEDIATE SOURCE:
  - (A) LIBRARY: CONUTUT01
  - (B) CLONE: 2504333

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Ala	Ala	Glu	Asp	Val	Val	Ala	Thr	Gly	Ala	Asp	Pro	Ser	Asp	Leu
1				5					10					15	
Glu	Ser	Gly	Gly	Leu	Leu	His	Glu	Ile	Phe	Thr	Ser	Pro	Leu	Asn	Leu
			20					25						30	

Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly  
 35 40 45  
 Asp Gln Pro Ala Ala Ser Gly Asp Arg Thr Thr Thr Xaa Pro Pro Pro  
 50 55 60  
 Leu Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro Ala Glu Leu Arg Arg  
 65 70 75 80  
 Phe Asp Gly Val Gln Asp Pro Arg Ile Leu Met Ala Ile Asn Gly Lys  
 85 90 95  
 Val Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr Gly Pro Glu Gly Pro  
 100 105 110  
 Tyr Gly Val Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe  
 115 120 125  
 Cys Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr Asp Asp Leu Ser Asp  
 130 135 140  
 Leu Thr Ala Ala Gln Gln Glu Thr Leu Ser Asp Trp Glu Ser Gln Phe  
 145 150 155 160  
 Thr Phe Lys Tyr His His Val Gly Lys Leu Leu Lys Glu Gly Glu Glu  
 165 170 175  
 Pro Thr Val Tyr Ser Asp Glu Glu Glu Pro Lys Asp Glu Ser Ser Arg  
 180 185 190  
 Lys Asn Val Lys Ala Phe Ser Gly Ser Ile Ser Xaa Xaa Tyr Phe Ala  
 195 200 205  
 Lys Ser Phe Val Thr Val His Xaa Val Phe Lys Thr  
 210 215 220

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 788 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: CONUTUT01  
 (B) CLONE: 2504333

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCCGCCGAAC	CCCGCGCGCC	ACTCGCTCGC	TCAGAGGGAG	GAGAAAGTGG	CGAGTTCGG	60
ATCCCTGCCT	AGCGCGGCC	AACCTTTACT	CCAGAGATCA	TGGCTGCCGA	GGATGTGGTG	120
GCGACTGGCG	CCGACCCAAG	CGATCTGGAG	AGCGGCGGGC	TGCTGCATGA	GATTTTCACG	180
TCGCCGCTCA	ACCTGCTGCT	GCTTGGCCTC	TGCATCTTCC	TGCTCTACAA	GATCGTGCGC	240
GGGGACCAGC	CGGCGGCCAG	CGGCGACAGG	ACGACGACGA	NGCCGCCCCC	TCTGCCCCGC	300
CTCAAGCGGC	GCGACTTCAC	CCCCGCCGAG	CTGCGGCGCT	TCGACGGCGT	CCAGGACCCG	360
CGCATACTCA	TGGCCATCAA	CGGCAAGGTG	TTCGATGTGA	CCAAAGGCCG	CAAATTCTAC	420
GGGCCCCGAG	GGCCGTATGG	GGTCTTTGCT	GGAAGAGATG	CATCCAGGGG	CCTTGCCACA	480
TTTTGCCTGG	ATAAGGAAGC	ACTGAAGGAT	GAGTACGATG	ACCTTTCTGA	CCTCACTGCT	540
GCCCAGCAGG	AGACTCTGAG	TGACTGGGAG	TCTCAGTTCA	CTTTCAAGTA	TCATCACGTG	600
GGCAAACCTG	TGAAGGAGGG	GGAGGAGCCC	ACTGTGTACT	CAGATGAGGA	AGAACCAAAA	660
GATGAGAGTT	CCCGGAAAAA	TGTTAAAGCA	TTCAGTGGAA	GTATATCTAT	NNTGTATTTT	720
GCAAATCAT	TTGTAACAGT	CCACTNTGTC	TTTAAAACAT	AGTGTTACAA	TATTTAGAAA	780
GTTTGAGC						788

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank  
 (B) CLONE: 1518818

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala Asp Pro Ser Glu Leu
 1          5          10          15
Glu Gly Gly Gly Leu Leu Gln Glu Ile Phe Thr Ser Pro Leu Asn Leu
          20          25          30
Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly
          35          40          45
Asp Gln Pro Gly Ala Ser Gly Asp Asn Asp Asp Glu Pro Pro Pro
          50          55          60
Leu Pro Arg Leu Lys Pro Arg Asp Phe Thr Pro Ala Glu Leu Arg Arg
          65          70          75          80
Tyr Asp Gly Val Gln Asp Pro Arg Ile Leu Met Ala Ile Asn Gly Lys
          85          90          95
Val Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr Gly Pro Glu Gly Pro
          100          105          110
Tyr Gly Val Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe
          115          120          125
Cys Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr Asp Asp Leu Ser Asp
          130          135          140
Leu Thr Pro Ala Gln Gln Glu Thr Leu Asn Asp Trp Asp Ser Gln Phe
          145          150          155          160
Ser Ser Pro Ser Ser Thr Ile Thr Trp Gly Lys Leu Leu Glu Gly Ala
          165          170          175
Glu Glu Pro Ile Val Tyr Ser Asp Asp Glu Glu Gln Lys Met Arg Leu
          180          185          190
Leu Gly Arg Val Thr Glu Ala Val Ser Gly Ala Tyr Leu Phe Leu Tyr
          195          200          205
Phe Ala Lys Ser Phe Val Thr Phe Gln Ser Val Phe Thr Thr Trp
          210          215          220

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## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1657409

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Ala Ala Glu Asp Val Ala Ala Thr Gly Ala Asp Pro Ser Glu Leu
 1          5          10          15
Glu Gly Gly Gly Leu Leu His Glu Ile Phe Thr Ser Pro Leu Asn Leu
          20          25          30
Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly
          35          40          45
Asp Gln Pro Ala Ala Ser Asp Ser Asp Asp Glu Pro Pro Pro Leu
          50          55          60
Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro Ala Glu Leu Arg Arg Phe
          65          70          75          80
Asp Gly Val Gln Asp Pro Arg Ile Leu Met Ala Ile Asn Gly Lys Val
          85          90          95
Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr Gly Pro Glu Gly Pro Tyr
          100          105          110
Gly Val Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe Cys
          115          120          125
Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr Asp Asp Leu Ser Asp Leu
          130          135          140
Thr Pro Ala Gln Gln Glu Thr Leu Asn Asp Trp Asp Ser Gln Phe Thr
          145          150          155          160
Phe Lys Tyr His His Val Gly Lys Leu Leu Lys Glu Gly Glu Glu Pro
          165          170          175
Thr Val Tyr Ser Asp Glu Glu Glu Pro Lys Asp Glu Ser Ala Arg Lys
          180          185          190

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